RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: [

Source:

Date Processed by STIC:

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Hilton, Douglas J.
      5
            (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
      7
           (iii) NUMBER OF SEQUENCES: 25
      9
            (iv) CORRESPONDENCE ADDRESS:
     11
                  (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
     13
                  (B) STREET: 400 Garden City Plaza
     14
                  (C) CITY: Garden City
     15
                   (D) STATE: New York
     16
                  (E) COUNTRY: United States of America
     17
                  (F) ZIP: 11530
     18
             (v) COMPUTER READABLE FORM:
     20
                  (A) MEDIUM TYPE: Floppy disk
     22
                   (B) COMPUTER: IBM PC compatible
     23
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     24
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     25
            (vi) CURRENT APPLICATION DATA:
     27
                  (A) APPLICATION NUMBER: US/09/532,263A
C--> 29
                  (B) FILING DATE: 22-Mar-2000
C--> 30
                  (C) CLASSIFICATION:
     31
          (viii) ATTORNEY/AGENT INFORMATION:
     33
                  (A) NAME: Presser, Leopold
     35
                  (B) REGISTRATION NUMBER: 19,827
     36
     37
                  (C) REFERENCE/DOCKET NUMBER: 10296
            (ix) TELECOMMUNICATION INFORMATION:
     39
                   (A) TELEPHONE: (516) 742-4343
     41
                   (B) TELEFAX: (516) 742-4366
     42
                  (C) TELEX: 203 901 SANS UR
     43
     45 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     47
     49
                  (A) LENGTH: 5 amino acids
                   (B) TYPE: amino acid
     50
                   (C) STRANDEDNESS: single
     51
     52
                   (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: DNA (genomic)
     56
            (ix) FEATURE:
                  (A) NAME/KEY: misc feature
     57
     58
                   (B) LOCATION: 3..3
                   (D) OTHER INFORMATION: /note= "Xaa at Position 3 is any amino acid"
     59
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     61
             Trp Ser Xaa Trp Ser
  -> 63
     64
```

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt
Output Set: N:\CRF4\03302005\1532263A.raw

66 (2) INFORMATION FOR SEQ ID NO: 2: 68 (i) SEQUENCE CHARACTERISTICS: 70 (A) LENGTH: 1705 base pairs 71 (B) TYPE: nucleic acid 72 (C) STRANDEDNESS: single 73 (D) TOPOLOGY: linear	
75 (ii) MOLECULE TYPE: DNA (genomic)	
77 (ix) FEATURE:	
79 (A) NAME/KEY: CDS	
80 (B) LOCATION: 451340	
82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
84 GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC	. 56
85 Met Ser Ser Ser	
86 1	104
88 TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG	104
89 Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val	
90 5 10 15 20	152
92 TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG	152
93 Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln 94 25 30 35	
94 25 30 35 96 TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT	200
97 Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser	200
98 40 45 50	
100 GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC	248
101 Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu	210
101 Ala Gly IIII F10 val Bel 11p The Alg Abp Gly Abp Bel Alg Bed 200	
102 104 CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG	296
105 Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val	
106 70 75 80	
108 GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA	344
109 Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val	
110 85 90 95 100	
112 TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT	392
113 Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro	
114 105 110 115	
116 GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG	440
117 Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp	
118 120 125 130	
120 AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC	488
121 Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr	
122 135 140 145	
124 AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC	536
125 Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser	
126 150 155 160	F04
128 ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT	584
129 Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys	
130 165 170 175 180	622
132 GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC	632
133 Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr	

RAW SEQUENCE LISTING

DATE: 03/30/2005 32,263A TIME: 10:35:32

PATENT APPLICATION: US/09/532,263A TIME: 10

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

134					185					190					195		
136	GAG	GTG	AAC	CCA	CTG	GGT	GCC	AGC	ACG	TGC	CTA	CTG	GAT	GTG	AGA	TTA	680
															Arg		
138				200		•			205	•			-	210			
	CAG	AGC	ATC		CGT	CCT	GAT	CCA	CCC	CAA	GGA	CTG	CGG	GTG	GAA	TCC	728
															Glu		
142	0111	501	215				p	220			1		225				
	CTA	ССТ		TAC	CCG	ΔGΔ	CGC		САТ	GCC	AGC	TGG		TAC	CCT	GCC	776
															Pro		
	vaı		Gry	ı yı	FIO	Arg	235	пси	111.5	niu	DCI	240	****	-1-			
146	maa	230	CCT	ccc	CNN	CCC		արա	СТС	CTC	AAG		CGG	ттс	CAA	ጥልሮ	824
															Gln		021
		пр	Arg	Arg	GIII		птэ	FIIC	пеп	пеп	255	FIIC	Arg	шец	GIII	260	
	245	~~~	~~~	~~~	G 3 TF	250	000	maa	maa	7 00		ana.	000	א תיתי	ccc		872
															GGC		072
	Arg	Pro	Ala	GIN		Pro	Ата	ттр	ser		vaı	GIU	PLO	TIE	Gly 275	ьeu	
154					265		~~=	~=~	a a m	270	ama	007	a	aaa		CCA	920
															GTA		920
	Glu	Glu	Val		Thr	Asp	Ala	Val		GLY	ьeu	Pro	His		Val	Arg	
158				280					285					290			0.50
															TGG		968
161	Val	Ser	Ala	Arg	Asp	Phe	Leu		Ala	Gly	Thr	Trp		Ala	Trp	Ser	
162			295					300					305				
															GAG		1016
165	Pro	Glu	Ala	\mathtt{Trp}	Gly	Thr	Pro	Ser	Thr	Gly	Pro	Leu	Gln	Asp	Glu	Ile	
166		310					315					320					
															GTA		1064
169	Pro	Asp	Trp	Ser	Gln	Gly	His	Gly	Gln	Gln	Leu	Glu	Ala	Val	Val	Ala	
	325					330					335					340	
															GAC		1112
172	Gln	Glu	Asp	Ser	Pro	Ala	Pro	Ala	Arg	Pro	Ser	Leu	Gln	Pro	Asp	Pro	
173					345					350					355		
															TTA		1160
176	Arg	Pro	Leu	Asp	His	Arg	Asp	Pro	Leu	Glu	Gln	Val	Ala	Val	Leu	Ala	
177				360					365					370			
179	TCT	CTG	GGA	ATC	TTC	TCT	TGC	CTT	GGC	CTG	GCT	GTT	GGA	GCT	CTG	GCA	1208
180	Ser	Leu	Gly	Ile	Phe	Ser	Cys	Leu	Gly	Leu	Ala	Val	Gly	Ala	Leu	Ala	
181			375					380					385				
183	CTG	GGG	CTC	TGG	CTG	AGG	CTG	AGA	CGG	AGT	GGG	AAG	GAT	GGA	CCG	CAA	1256
															Pro		
		390		-		_	395	_	_		_	400					
187	AAA	CCT	GGG	CTC	TTG	GCA	CCC	ATG	ATC	CCG	GTG	GAA	AAG	CTT	CCA	GGA	1304
																Gly	
	405	-				410					415		_			420	
	ATT	CCA	AAC	CTG	CAG	AGG	ACC	CCA	GAG	AAC	TTC	AGC	TGA'	TTTC	ATC		1350
	Ile																
193					425	ر				430							
		AACC	CGG '	TCAG:		GG G	GCAG	AAAG	A GG		GCAG	TGG	ATCC	CTG	TGGA	TGGAGG	1410
																CCGGCT	1470
																TACAGA	1530
エジラ	CUM					11											

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

201	እርጥር	יייבייני	מייים כ	יריתנים	ነጋልጥ(ים דים	:ጥር:ጥር	ነጥ ልጥር	ב ידוכיו	GAC	AGGG	AGCZ	ΑΑΑ	TT (тстс	CATGT	1590
																GTGAA	
						CG GF											1705
						SEQ											
207	(2)					iarac											
211		(1)		-		1: 43				ic.							
211						amir			uci								
213						OGY:											
		(;;)	•	•		PE:											
215 217						SCRI	-		E O I	ות מו) · 3 ·						
	Mot					Ser							Val	Ala	Val	Ala	
220	1	Ser	Der	DCI	5	DCI	O ₁	шец		10		200			15		
		Δ7 =	T.611	Val	_	Ser	Ser	Ser	Pro		Pro	Gln	Ala	Trp		Pro	
223	1111	nια	шси	20	001	501		001	25	07.0				30	2		
	Pro	Glv	Val		Tvr	Gly	Gln	Pro		Ara	Pro	Val	Met		Cvs	Cvs	
226		017	35	·	-1-	0-1		40	1	5			45		•	•	
	Pro	Glv		Ser	Ala	Gly	Thr		Val	Ser	Trp	Phe	Arq	Asp	Gly	Asp	
229		50				1	55				-	60	_	_	•	-	
	Ser		Leu	Leu	Gln	Gly		Asp	Ser	Gly	Leu	Gly	His	Arg	Leu	Val	
232	65	5				70		-		•	75	-		_		80	
		Ala	Gln	Val	Asp	Ser	Pro	Asp	Glu	Gly	Thr	Tyr	Val	Cys	Gln	Thr	
235					85			-		90		-		_	95		
	Leu	Asp	Gly	Val	Ser	Gly	Gly	Met	Val	Thr	Leu	Lys	Leu	Gly	Phe	Pro	
238		_	•	100		_	_		105					110			
240	Pro	Ala	Arg	Pro	Glu	Val	Ser	Cys	Gln	Ala	Val	Asp	Tyr	Glu	Asn	Phe	
241			115					120					125				
243	Ser	Cys	Thr	Trp	Ser	Pro	Gly	Gln	Val	Ser	Gly	Leu	Pro	Thr	Arg	Tyr	
244		130					135					140					
246	Leu	Thr	Ser	Tyr	Arg	Lys	Lys	Thr	Leu	Pro	Gly	Ala	Glu	Ser	Gln		
	145					150					155	_		_	_	160	
	Glu	Ser	Pro	Ser		Gly	Pro	Trp	Pro		Pro	Gln	Asp	Pro		Glu	
250					165				_	170		_			175	_	
252	Ala	Ser	Arg		Val	Val	His	Gly		Glu	Phe	Trp	Ser		Tyr	Arg	
253			_	180			_	_	185			_	1	190	•	T	
	Ile	Asn		Thr	Glu	Val	Asn		Leu	GIA	Ala	ser		Cys	ьeu	Leu	
256		_	195	_		_		200	_	_		_	205	~ 1	a 1	T	
	Asp		Arg	Leu	Gln	Ser		Leu	Arg	Pro	Asp		Pro	GIn	GIĀ	ьeu	
259		210		_		_	215		_	_	_	220	***		0	m	
	_	Val	Glu	Ser	Val	Pro	GIY	Tyr	Pro	Arg		ьeu	HIS	Ala	ser		
	225	_	_		_	230	_	_	~7	_	235	731	.	.	T	240	
	Thr	Tyr	Pro	Ala		Trp	Arg	Arg	GIn		HIS	Pne	ьeu	ьeu		Pne	
265	_	_	~7	_	245	,		01	77.	250 D	77-	Шеле	Com	mb =	255	Clu	
	Arg	Leu	GIn		Arg	Pro	Ата	GIn		Pro	Ата	пр	ser			GIU	
268	-		~ 3	260	G 3	03 -	77 T	T7.	265	7	77 ~	17~ T	7. T. C.	270		Dro	
	Pro	тте		ьeu	GIU	Glu	vaı		TUL	Asp	ATG	vaı		GTĀ	ъeи	FIO	
271	**.		275	3	TT - 7	0	77 -	280	7 ~	Db.c	T 01-	7 ~~	285	C1	ть∽	Пъъ	
			vaı	arg	val	Ser		Arg	Asp	rne	ьeu		MIG	GTÄ	TIII	тър	
274		290	m	0	Desc	C1	295	Т	C1	ሞኤ ∽	D~c	300	ጥኮ~	Gl v	Dro	T.011	
276	ser	ата	ırp	ser	PIO	Glu	AId	ттЪ	GTÅ	TIIT	FIO	Set	TIIT	GIY		11 C U	

RAW SEQUENCE LISTING DATE: 03/30/2005
PATENT APPLICATION: US/09/532,263A TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

277																	
						310					315					320	
279	Gln	Asp	Glu	Ile	Pro	Asp	Trp	Ser	Gln	Gly	His	Gly	Gln	Gln	Leu	Glu	
280					325					330					335		
282	Ala	Val	Val	Ala	Gln	Glu	Asp	Ser	Pro	Ala	Pro	Ala	Arg	Pro	Ser	Leu	
283				340			_		345					350			
	Gln	Pro	Asp		Ara	Pro	Leu	Asp	His	Ara	Asp	Pro	Leu	Glu	Gln	Val	
286	02		355		5			360			•		365				
	λla	Val		Δla	Ser	T.e11	Glv		Phe	Ser	Cvs	Leu		Leu	Ala	Val	
289	ALG	370	шси	niu	DCI	шси	375				0,0	380	1				
	C111		T.011	7] a	T.011	Glv		Trn	T.e.11	Δrσ	T.e11	Arg	Ara	Ser	Glv	Lvs	
	_	AIG	пеп	AIG	шец	390	шеи	ııp	шси	9	395		-,9	-	U-1	400	
292		C1	Dro	Cln	Tarc		Gl v	T.611	T.A11	Δla		Met	Tle	Pro	Val		
	Asp	Gry	PIO	GIII	405	FIO	Gry	шец	пец	410	110	1100	110	110	415	014	
295	•	T	7	01		Dwo	7 ~~	T 011	C1 n		Thr	Dro	Clu	Nan		Ser	
	гуѕ	Leu	Pro	_	TTE	PLO	ASII	neu		Arg	1111	Pro	Gru		FIIC	Der	
298	4 = 1			420				••	425					430			
	(2)						ID 1										
303		(i)					CTERI										
305							300 k		_	:s							
306							leic										
307							ESS:	_	gle								,
308			(1) T(OPOL	OGY:	line	ear									
310		(ii)	MOI	LECUI	LE T	PE:	CDN	Ą									
312		(iii)	HYI	POTH	ETIC	AL: 1	10										
314		(iv)	AN'	ri-si	ENSE	: NO											
317		(ix)) FE	ATURI	Ξ:												
319			(2	A) NA	AME/I	KEY:	CDS										
320			/1	2 \ T.	ንሮልጥ	ON:	128	139	96								
			/1	<i>) 1</i> 10													
322		(xi)					PTIC	ON: S	SEQ :	D NO): 4	:					
	TCT) SE	QUEN	CE DI	ESCR:	PTI						GAAG	CCT (CAGT"	rttgga	60
324		AACA	SEC	QUENC CTAC	CE DI	ESCR:	PTIC GGTGC	CATC	A AT	CTTTC	CTCC	TAG				TTTGGA CCTCTC	60 120
324 326	GAG	AACA(BAAG)) SE(GCC : AGC (QUENC TTACC CAGG	CE DI CCCA(CTTT	ESCRI CT TO AG CI	PTIC GGTGC PCCC	CATCI ATCT	A AT	CTTTC GGTC	CTCC CGGG	TAGG GAT	TTTT(GAC '	rcta(CCTCTC	
324 326 328	GAG	AACA(BAAG)	SE(GCC : AGC (ATG	QUENC TTACC CAGGC AGC	CE DI CCCA CTTTI AGC	ESCRI CT TO AG CI AGC	PTIC GTGC CCC! TGC	CATCI ATCT TCA	A AT" C AGG GGG	TTTT(GGT(CTG	CTCC CGGG AGC	TAGG GAT AGG	GTC	GAC '	CTA GTG	CCTCTC GCC	120
324 326 328 329	GAG	AACA(BAAG)	SE(GCC S AGC (ATG Met	QUENC TTACC CAGGC AGC	CE DI CCCA CTTTI AGC	ESCRI CT TO AG CI AGC	PTIC GTGC CCC! TGC	CATCI ATCT TCA	A AT" C AGG GGG	TTTT(GGT(CTG	CTCC CGGG AGC	TAGG GAT	GTC	GAC '	CTA GTG	CCTCTC GCC	120
324 326 328 329 330	GAGO CCC	AACA(BAAG) ACAG	SEC SCC S AGC C ATG Met	QUENC CAGG AGC Ser	CE DI CCCA CTTTI AGC Ser	ESCR: CT TO AG CT AGC Ser	PTIC GGTGC TCCC! TGC Cys 5	CATCA ATCTO TCA Ser	A ATT C AGG GGG Gly	TTTT(GGGT(CTG Leu	CTCC CGGG AGC Ser	TAGG GATT AGG Arg 10	GTC Val	GAC ' CTG Leu	GTG Val	CCTCTC GCC Ala	120
324 326 328 329 330 332	GAGO CCCA GTG	AACAG BAAGA ACAG GCT	SE(GCC TAGC (AGC (ATG Met 1 ACA	QUENC TTACC CAGGC AGC Ser GCC	CE DI CCCAC CTTTI AGC Ser CTG	ESCR: CT TO AG C' AGC Ser GTG	PTIO GGTGO TGC TGC Cys 5 TCT	CATCA ATCTO TCA Ser GCC	A ATT C AGG GGG Gly TCC	TTTT(GGT(CTG Leu TCC	CTCC CGGG AGC Ser	TAGG GATT AGG Arg 10 TGC	TTTT(GTC Val CCC	GAC ' CTG Leu CAG	CTA GTG Val GCC	CCTCTC GCC Ala TGG	120 169
324 326 328 329 330 332 333	GAGG CCCA GTG Val	AACAG BAAGA ACAG GCT	SE(GCC TAGC (AGC (ATG Met 1 ACA	QUENC TTACC CAGGC AGC Ser GCC	CE DI CCCAC CTTTI AGC Ser CTG	ESCRI CT TO AG CT AGC Ser GTG Val	PTIO GGTGO TGC TGC Cys 5 TCT	CATCA ATCTO TCA Ser GCC	A ATT C AGG GGG Gly TCC	TTTT(GGT(CTG Leu TCC	CTCC CGGG AGC Ser CCC Pro	TAGG GATT AGG Arg 10	TTTT(GTC Val CCC	GAC ' CTG Leu CAG	CTA GTG Val GCC	CCTCTC GCC Ala TGG	120 169
324 326 328 329 330 332 333 334	GAGG CCCA GTG Val 15	AACAG BAAGA ACAG GCT Ala	SE(C) AGC (ATG) ATG Met 1 ACA	QUENC TTACC CAGGC AGC Ser GCC Ala	CE DI CCCA CTTTA AGC Ser CTG Leu	ESCRI CT TO AG CI AGC Ser GTG Val 20	IPTIC GGTGC TGC TGC Cys 5 TCT Ser	CATCA ATCTO TCA Ser GCC Ala	A ATT GGG GGG Gly TCC Ser	TTTT(GGGT(CTG Leu TCC Ser	CTCC CGGG AGC Ser CCC Pro 25	TAGG GATT AGG Arg 10 TGC Cys	TTTTC GTC Val CCC Pro	GAC ' CTG Leu CAG Gln	CTAC GTG Val GCC Ala	CCTCTC GCC Ala TGG Trp 30	120 169
324 326 328 329 330 332 333 334 336	GAGG CCCZ GTG Val 15 GGC	AACAG ACAG GCT Ala	SECC AGC ATG Met 1 ACA Thr	QUENC CAGGC AGC Ser GCC Ala	CE DI CCCAC CTTTA AGC Ser CTG Leu	ESCRI CT TO AG CT AGC Ser GTG Val 20 CAG	EPTIC GGTGC TGC TGC Cys 5 TCT Ser	CATCA ATCTO TCA Ser GCC Ala	A ATT GGG GGG Gly TCC Ser	CTTTC CTG CTG Leu TCC Ser	CTCC CGGG AGC Ser CCC Pro 25 GGC	TAGG GATT AGG Arg 10 TGC Cys	GTC Val CCC Pro	GAC CTG Leu CAG Gln GTG	CTAC GTG Val GCC Ala	CCTCTC GCC Ala TGG Trp 30 CTG	120 169 217
324 326 328 329 330 332 333 334 336 337	GAGG CCCZ GTG Val 15 GGC	AACAG ACAG GCT Ala	SECC AGC ATG Met 1 ACA Thr	QUENC CAGGC AGC Ser GCC Ala	CE DI CCCAC CTTTA AGC Ser CTG Leu GTC Val	ESCRI CT TO AG CT AGC Ser GTG Val 20 CAG	EPTIC GGTGC TGC TGC Cys 5 TCT Ser	CATCA ATCTO TCA Ser GCC Ala	A ATT GGG GGG Gly TCC Ser	TTTTC GGGTC CTG Leu TCC Ser CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC	TAGG GATT AGG Arg 10 TGC Cys	GTC Val CCC Pro	GAC CTG Leu CAG Gln GTG	GTG Val GCC Ala AAG	CCTCTC GCC Ala TGG Trp 30 CTG	120 169 217
324 326 328 329 330 332 333 334 336 337 338	GAGG CCCZZ GTG Val 15 GGC Gly	AACAG ACAG GCT Ala CCC Pro	SE() SE() AGC () ATG Met 1 ACA Thr CCA	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly	CE DI CCCAC CTTTA AGC Ser CTG Leu GTC Val	ESCR: AG CT AG C AGC Ser GTG Val 20 CAG Gln	EPTIC GGTGC TGC Cys 5 TCT Ser TAT Tyr	CATCA TCA Ser GCC Ala GGG Gly	A ATT C AGC GGG Gly TCC Ser CAG	TTTTC CTG Leu TCC Ser CCA Pro 40	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GAT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val	GTG Val GCC Ala AAG Lys 45	CCTCTC GCC Ala TGG Trp 30 CTG Leu	120 169 217 265
324 326 328 329 330 332 333 334 336 337 338 340	GAGG CCCZ GTG Val 15 GGC Gly	AACAG GAAGA ACAG GCT Ala CCC Pro	SECC SAGC (ATG Met 1 ACA Thr CCA Pro	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly	CE DI CCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG	ESCR: AG CT AG CT Ser GTG Val 20 CAG Gln	EPTICEGTGG FCCCZ TGC Cys 5 TCT Ser TAT Tyr	CATCA TCA Ser GCC Ala GGG Gly	A ATT C AGG GGG Gly TCC Ser CAG Gln	TTTTC CTG Leu TCC Ser CCA Pro 40 CCA	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GATT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val	GTG Val GCC Ala AAG Lys 45 CGG	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT	120 169 217
324 326 328 329 330 332 333 334 336 337 338 340 341	GAGG CCCZ GTG Val 15 GGC Gly	AACAG GAAGA ACAG GCT Ala CCC Pro	SECC SAGC (ATG Met 1 ACA Thr CCA Pro	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly GGA Gly	CE DI CCCAC CTTTA AGC Ser CTG Leu GTC Val 35 GTG	ESCR: AG CT AG CT Ser GTG Val 20 CAG Gln	EPTICEGTGG FCCCZ TGC Cys 5 TCT Ser TAT Tyr	CATCA TCA Ser GCC Ala GGG Gly	A ATT G AGG GGG Gly TCC Ser CAG Gln GAC Asp	TTTTC CTG Leu TCC Ser CCA Pro 40 CCA	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly	TAGG GAT AGG Arg 10 TGC Cys AGG Arg	GTC Val CCC Pro TCC Ser	CTG Leu CAG Gln GTG Val TTT Phe	GTG Val GCC Ala AAG Lys 45 CGG	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT	120 169 217 265
324 326 328 329 330 332 333 334 336 337 338 340 341 342	GAGG CCCZ GTG Val 15 GGC Gly TGT Cys	GCT ACAC GCT Ala CCC Pro	SECC SAGC (ATG Met 1 ACA Thr CCA Pro	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly GGA Gly 50	CE DI CCCAC CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val	ESCR: AG CT AG CT Ser GTG Val 20 CAG Gln ACT	TAT TYr	CATCA ATCTO TCA Ser GCC Ala GGG Gly GGG Gly	A ATT G AGG GGG Gly TCC Ser CAG Gln GAC Asp	TTTTC GGGTC Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC Ser	GTC Val CCC Pro TCC Ser TGG Trp	CTG Leu CAG Gln GTG Val TTT Phe 60	GCC Ala AAG Lys CGG Arg	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265 313
324 326 328 329 330 332 333 334 336 337 338 340 341 342 344	GAGG CCCZ GTG Val 15 GGC Gly TGT Cys	GCT Ala CCC Pro TGT Cys	SECC SAGC (ATG Met 1 ACA Thr CCA Pro CCT Pro CCA	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG	CE DI CCCAC CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val	ESCR: AG CT AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	EPTICEGTGG TCCCZ TGC Cys 5 TCT Ser TAT Tyr GCC Ala	TCA Ser GCC Ala GGG Gly GGG GGA	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC ser	GTC Val CCC Pro TCC Ser TGG Trp CTA	CAG Gln GTG Val TTT Phe 60 GGG	GCC Ala AAG Lys 45 CGG Arg	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265
324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345	GAGG CCCZ GTG Val 15 GGC Gly TGT Cys	GCT Ala CCC Pro TGT Cys	SECC CACCACCACCACCACCACCACCACCACCACCACCACC	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG	CE DI CCCAC CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val	ESCR: AG CT AG CT AGC Ser GTG Val 20 CAG Gln ACT Thr	EPTICEGTGG TCCCZ TGC Cys 5 TCT Ser TAT Tyr GCC Ala	CATCA ATCTO TCA Ser GCC Ala GGG Gly GGG Gly	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC ser	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu	CAG Gln GTG Val TTT Phe 60 GGG	GCC Ala AAG Lys 45 CGG Arg	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp	120 169 217 265 313
324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346	GAGG CCCI GTG Val 15 GGC Gly TGT Cys GGG Gly	GCT ALA CCC Pro TGT Cys GAG Glu	SECC SAGC (ATG Met 1 ACA Thr CCA Pro CCT Pro 65	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly 50 AAG Lys	CE DI CCCAC CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu	ESCR: CT TC AG C' AGC Ser GTG Val 20 CAG Gln ACT Thr	TAT TYP GCC Ala	GATCA TCA Ser GCC Ala GGG Gly GGA Gly 70	GAC ASP CCT CCT CAG CAC CAC CAC CCT	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro GAC Asp	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCC Ala AAG Lys CGG Arg CAT	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu	120 169 217 265 313
324 326 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348	GAGG CCCI GTG Val 15 GGC Gly TGT Cys GGG Gly	GCT Ala CCC Pro TGT Cys GAG GIU	SECC CACCA CCA Pro CCA Pro CCA CTG	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly 50 AAG Lys	CE DI CCCAG CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu	ESCR: CT TC AG C' AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu	TAT TYP GCC Ala GAC	CATCA ATCTO TCA Ser GCC Ala GGG Gly GGA Gly 70 AGC	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT Pro	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro GAC Asp	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser	TAGG GATT AGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCC Ala AAG Lys CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313
324 328 329 330 332 333 334 336 337 342 342 344 345 346 348 349	GAGG CCCI GTG Val 15 GGC Gly TGT Cys GGG Gly	GCT Ala CCC Pro GAG Glu GTC Val	SECC CACCA CCA Pro CCA Pro CCA CTG	QUENC TTACC CAGGC AGC Ser GCC Ala GGG Gly 50 AAG Lys	CE DI CCCAG CTTTZ AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu	ESCR: CT TC AG C' AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu	TPTICE GGTGC TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp	CATCA ATCTO TCA Ser GCC Ala GGG Gly GGA Gly 70 AGC	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT Pro	TTTTC GGGTC CTG Leu TCC Ser CCA Pro 40 CCA Pro GAC Asp	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC	CAG Gln GTG Val TTT Phe 60 GGG Gly	GCC Ala AAG Lys CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313
324 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348 349 350	GAGG CCCI GTG Val 15 GGC Gly TGT Cys GGG Gly CTG Leu	GCT Ala CCC Pro GAG Glu GTC Val 80	SECC CACCA CCA Pro Leu	GUENG CAGGG AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG Lys GCC Ala	CE DICCCAGE CCCAGE AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu CAG Gln	ESCR: CT TC AG C' AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA Ala	EPTICEGTGG FCCCZ TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp 85	GATCA TCA Ser GCC Ala GGG Gly GGA Gly 70 AGC Ser	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT Pro ACT	TTTTCGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser GAG Glu	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly 90	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC Thr	CAG Gln GTG Val TTT Phe 60 GGG Gly TAC	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC Cys	120 169 217 265 313 361 409
324 328 329 330 332 333 334 336 337 338 340 341 342 344 345 346 348 349 350	GAGG CCCI GTG Val 15 GGC Gly TGT Cys GGG Gly CTG Leu	GCT Ala CCC Pro GAG Glu GTC Val 80	SECC CACCA CCA Pro Leu	GUENG CAGGG AGC Ser GCC Ala GGG Gly GGA Gly 50 AAG Lys GCC Ala	CE DICCCAGE CCCAGE AGC Ser CTG Leu GTC Val 35 GTG Val CTG Leu CAG Gln	ESCR: CT TC AG C' AGC Ser GTG Val 20 CAG Gln ACT Thr CTC Leu GCA Ala	EPTICEGTGG FCCCZ TGC Cys 5 TCT Ser TAT Tyr GCC Ala CAG Gln GAC Asp 85	GATCA TCA Ser GCC Ala GGG Gly GGA Gly 70 AGC Ser	A ATT C AGG GGG Gly TCC Ser CAG Gln GAC Asp 55 CCT Pro ACT	TTTTCGGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	CTCC CGGG AGC Ser CCC Pro 25 GGC Gly GTG Val TCT Ser GAG Glu	TAGG GATTAGG Arg 10 TGC Cys AGG Arg TCC Ser GGG Gly 90	TTTTC GTC Val CCC Pro TCC Ser TGG Trp CTA Leu 75 ACC Thr	CAG Gln GTG Val TTT Phe 60 GGG Gly TAC	GCC Ala AAG Lys 45 CGG Arg CAT His	CCTCTC GCC Ala TGG Trp 30 CTG Leu GAT Asp GAA Glu TGC	120 169 217 265 313

RAW SEQUENCE LISTING ERROR SUMMARY DATENT APPLICATION: US/09/532,263A

DATE: 03/30/2005 TIME: 10:35:33

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.3 \(\)
Seq#:8; N Pos. 7
Seq#:9; N Pos. 7
Seq#:23; N Pos. 7

VERIFICATION SUMMARY

DATE: 03/30/2005

PATENT APPLICATION: US/09/532,263A

TIME: 10:35:33

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0